1 ATGAGCCAGC CCAGGCCCCG CTACGTGGTA GACAGAGCCG CATACTCCCT 51 TACCCTCTTC GACGATGAGT TTGAGAAGAA GGACCGGACA TACCCAGTGG 101 GAGAGAAACT TCGCAATGCC TTCAGATGTT CCTCAGCCAA GATCAAAGCT 151 GTGGTGTTTG GGCTGCTGCC TGTGCTCTCC TGGCTCCCA AGTACAAGAT 201 TAAAGACTAC ATCATTCCTG ACCTGCTCGG TGGACTCAGC GGGGGATCCA 251 TCCAGGTCCC ACAAGGCATG GCATTTGCTC TGCTGGCCAA CCTTCCTGCA 301 GTCAATGGCC TCTACTCCTC CTTCTTCCCC CTCCTGACCT ACTTCTTCCT 351 GGGGGGTGTT CACCAGATGG TGCCAGGTAC CTTTGCCGTT ATCAGCATCC 401 TGGTGGGTAA CATCTGTCTG CAGCTGGCCC CAGAGTCGAA ATTCCAGGTC 451 TTCAACAATG CCACCAATGA GAGCTATGTG GACACAGCAG CCATGGAGGC 501 TGAGAGGCTG CACGTGTCAG CTACGCTAGC CTGCCTCACC GCCATCATCC 551 AGATGGGTCT GGGCTTCATG CAGTTTGGCT TTGTGGCCAT CTACCTCTCC 601 GAGTCCTTCA TCCGGGGCTT CATGACGGCC GCCGGCCTGC AGATCCTGAT 651 TTCGGTGCTC AAGTACATCT TCGGACTGAC CATCCCCTCC TACACAGGCC 701 CAGGGTCCAT CGTCTTTACC TTCATTGACA TTTGCAAAAA CCTCCCCCAC 751 ACCAACATCG CCTCGCTCAT CTTCGCTCTC ATCAGCGGTG CCTTCCTGGT 801 GCTGGTGAAG GAGCTCAATG CTCGCTACAT GCACAAGATT CGCTTCCCCA TCCCTACAGA GATGATTGTG GTGGTGGTGG CAACAGCTAT CTCCGGGGGC 901 TGTAAGATGC CCAAAAAGTA TCACATGCAG ATCGTGGGAG AAATCCAACG 951 CGGGTTCCCC ACCCCGGTGT CGCCTGTGGT CTCACAGTGG AAGGACATGA 1001 TAGGCACAGC CTTCTCCCTA GCCATCGTGA GCTACGTCAT CAACCTGGCT 1051 ATGGGCCGGA CCCTGGCCAA CAAGCACGGC TACGACGTGG ATTCGAACCA 1101 GGAGATGATC GCTCTCGGCT GCAGCAACTT CTTTGGCTCC TTCTTTAAAA 1151 TTCATGTCAT TTGCTGTGCG CTTTCTGTCA CTCTGGCTGT GGATGAGCT 1201 GGAGGAAAAT CCCAGGTGGC CAGCCTGTGT GTGTCTCTGG TGGTGATGAT 1251 CACCATGCTG GTCCTGGGGA TCTATCTGTA TCCTCTCCCT AAGTCTGTGC 1301 TAGGAGCCCT GATCGCTGTC AATCTCAAGA ACTCCCTCAA GCAACTCACC 1351 GACCCCTACT ACCTGTGGAG GAAGAGCAAG CTGGACTGTT GCATCTGGGT 1401 AGTGAGCTTC CTCTCCTCT TCTTCCTCAG CCTGCCCTAT GGTGTGGCAG 1451 TGGGTGTCGC CTTCTCCGTC CTGGTCGTGG TCTTCCAGAC TCAGTTTCGA 1501 AATGGCTATG CACTGGCCCA GGTCATGGAC ACTGACATTT ATGTGAATCC 1551 CAAGACCTAT AATAGGGCCC AGGATATCCA GGGGATTAAA ATCATCACGT 1601 ACTGCTCCCC TCTCTACTTT GCCAACTCAG AGATCTTCAG GCAAAAGGTC 1651 ATCGCCAAGA CTGTCTCCCT GCAGGAGCTG CAGCAGGACT TTGAGAATGC 1701 GCCCCCACC GACCCCAACA ACAACCAGAC CCCGGCTAAC GGCACCAGCG 1751 TGTCCTATAT CACCTTCAGC CCTGACAGCT CCTCACCTGC CCAGAGTGAG 1801 CCACCAGCCT CCGCTGAGGC CCCCGGCGAG CCCAGTGACA TGCTGGCCAG 1851 CGTCCCACCC TTCGTCACCT TCCACACCCT CATCCTGGAC ATGAGTGGAG 1901 TCAGCTTCGT GGACTTGATG GGCATCAAGG CCCTGGCCAA GCTGAGCTCC 1951 ACCTATGGGA AGATCGGCGT GAAGGTCTTC TTGGTGAACA TCCATGCCCA 2001 GGTGTACAAT GACATTAGCC ATGGAGGCGT CTTTGAGGAT GGGAGTCTAG 2051 AATGCAAGCA CGTCTTTCCC AGCATACATG ACGCAGTCCT CTTTGCCCAG 2101 GCAAATGCTA GAGACGTGAC CCCAGGACAC AACTTCCAAG GGGCTCCAGG 2151 GGATGCTGAG CTCTCCTTGT ACGACTCAGA GGAGGACATT CGCAGCTACT 2201 GGGACTTAGA GCAGGAGATG TTCGGGAGCA TGTTTCACGC AGAGACCCTG. 2251 ACCGCCCTGT GA (SEQ ID NO:1)

FEATURES:

JAN 1 5 2003

Start Codon: 1 Stop Codon: 2260



HOMOLOGOUS PROTEINS: Top BLAST Hite

TOP BLAST HITS:		
	Score	E
gb AAF81911.1 AF279265_1 (AF279265) putative anion transpor	476	e-133
gb AAF71715.1 AF230376_1 (AF230376) prestin [Meriones ungui	471	e-131
ref NP_000432.1 pendrin [Homo sapiens] >gi 11421915 ref XP	451	e-125
ref[NP_035997.1] Pendred syndrome homolog (human); Pendred'	448	e-124
ref[NP_062087.1 Pendred syndrome homolog (human) [Rattus n	447	e-124
ref[NP_067328.1 down-regulated in adenoma [Mus musculus] >	434	e-120
ref[NP_000102.1] down-regulated in adenoma protein [Homo sa	418	e-115
sp 070531 DTD_RAT SULFATE TRANSPORTER (DIASTROPHIC DYSPLASI	365	1e-99
ref[NP_000103.1 sulfate anion transporter 1; Diastrophic d	362	1e-98
ref[NP_031911.1 diastrophic dysplasia [Mus musculus] >gi 2	357	4e-97

BLAST to dbEST:

gi|8630793 /dataset=dbest /taxon=960...

Score

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:
Expression information from BLAST dbEST hits:
gi | 8630793 Human head-neck

1 MS
51 VV
101 VN
151 FN
201 ES

Docket No.: CL000861
Serial No.: 09/749,589
Inventors: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER...

```
1 MSQPRPRYVV DRAAYSLTLF DDEFEKKDRT YPVGEKLRNA FRCSSAKIKA 51 VVFGLLPVLS WLPKYKIKDY IIPDLLGGLS GGSIQVPQGM AFALLANLPA 101 VNGLYSSFFP LLTYFFLGGV HQMVPGTFAV ISILVGNICL QLAPESKFQV 151 FNNATNESYV DTAAMEAERL HVSATLACLT AIIQMGLGFM QFGFVAIYLS 201 ESFIRGFMTA AGLQILISVL KYIFGLTIPS YTGPGSIVFT FIDICKNLPH 251 TNIASLIFAL ISGAFLVLVK ELNARYMHKI RFPIPTEMIV VVVATAISGG 301 CKMPKKYHMQ IVGEIQRGFP TPVSPVVSQW KDMIGTAFSL AIVSYVINLA 351 MGRTLANKHG YDVDSNQEMI ALGCSNFFGS FFKIHVICCA LSVTLAVDGA 401 GGKSQVASLC VSLVVMITML VLGIYLYPLP KSVLGALIAV NLKNSLKQLT 451 DPYYLWRKSK LDCCIWVVSF LSSFFLSLPY GVAVGVAFSV LVVVFQTQFR 501 NGYALAQVMD TDIYVNPKTY NRAQDIQGIK IITYCSPLYF ANSEIFRQKV 551 IAKTVSLQEL QQDFENAPPT DPNNNQTPAN GTSVSYITFS PDSSSPAQSE 601 PPASAEAPGE PSDMLASVPP FVTFHTLILD MSGVSFVDLM GIKALAKLSS 651 TYGKIGVKVF LVNIHAQVYN DISHGGVFED GSLECKHVFP SIHDAVLFAQ 701 ANARDVTPGH NFQGAPGDAE LSLYDSEEDI RSYWDLEQEM FGSMFHAETL 751 TAL (SEQ ID NO:2)
```

FEATURES:

Functional domains and key regions:
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 3 1 153-156 NATN 2 156-159 NESY 3 580-583 NGTS

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site

Number of matches: 2 1 45-47 SAK 2 445-447 SLK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site

Number of matches: 2 1 7-15 RYVVDRAAY 2 447-454 KQLTDPYY



[5] PDOC00008 PS00008 MYRISTYL N-myristoylation site

Number of	matches:	10
1	77-82	GGLSGG
2	78-83	GLSGGS
3	89-94	GMAFAL
4	103-108	GLYSSF
5	335-340	GTAFSL
6	435-440	GALIAV
7	481-486	GVAVGV
8	485-490	GVAFSV
9	581-586	GTSVSY
10	681-686	GSLECK

Membrane	e spann	ing str	ucture	and domains:
Helix		End	Score	Certainty
1	51	71	0.893	Putative
2	82	102	1.020	Certain
3	107	127	1.729	Certain
4	130	150	1.497	Certain
5	186	206	1.723	Certain
6	228	248	1.517	Certain
7	256	276	1.898	Certain
8	288	308	1.252	Certain
9	338	358	1.568	Certain
10	383	403	1.304	Certain
11	412	432	2.345	Certain
12	469	489	1.997	Certain
13	619	639	1.146	Certain

JAN 15 2003 P.

Docket No.: CL000861
Serial No.: 09/749,589
Inventors: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER...

BLAST Alignment to Top Hit:
>gb|AAF81911.1|AF279265_1 (AF279265) putative anion transporter 1 [Homo sapiens]

Length = 738

Score = 476 bits (1224), Expect = e-133 Identities = 263/724 (36%), Positives = 428/724 (58%), Gaps = 36/724 (4%) Frame = +3LFDDEFEEKDR--TYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLL 227 Query: 54 L + EE R + P + R +CS A+ A++ LPVL WLP+Y ++D+++ DLL LNQEHLEELGRWGSAPRTHQWRTWLQCSRARAYALLLQHLPVLVWLPRYPVRDWLLGDLL 74 Sbjct: 15 Query: 228 GGLSGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVG 407 GLS +Q+PQG+A+ALLA LP V GLYSSF+P+ YF G + GTFAV+S++VG SGLSVAIMQLPQGLAYALLAGLPPVFGLYSSFYPVFIYFLFGTSRHISVGTFAVMSVMVG 134 Sbjct: 75 NICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVA 587 Query: 408 LAP+ A N+S ++ A +A R+ V++TL+ L + Q+GLG + FGFV SVTESLAPQ-----ALNDSMINETARDAARVQVASTLSVLVGLFQVGLGLIHFGFVV 186 Sbjct: 135 IYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASL 767 Query: 588 YLSE +RG+ TAA +Q+ +S LKY+FGL + S++GP S+++T +++C LP + ++ TYLSEPLVRGYTTAAAVQVFVSQLKYVFGLHLSSHSGPLSLIYTVLEVCWKLPQSKVGTV 246 Sbjct: 187 IFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIVGEIQ 947 Query: 768 + A ++G LV+VK LN + ++ PIP E++ ++ AT IS G + ++ + +VG I VTAAVAGVVLVVVKLLNDKLQQQLPMPIPGELLTLIGATGISYGMGLKHRFEVDVVGNIP 306 Sbjct: 247 Query: 948 RGFPTPVSPVVLQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSN 1127 PV+P + ++G+AF++A+V + I +++G+ A +HGY VDSNQE++ALG SN Sbjct: 307 AGLVPPVAPNTQLFSKLVGSAFTIAVVGFAIAISLGKIFALRHGYRVDSNQELVALGLSN 366 Query: 1128 FFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGA 1307 G F+ + C++S +L + GG SQVA SL +++ ++ LG + LPK+VL A LIGGIFQCFPVSCSMSRSLVQESTGGNSQVAGAISSLFILLIIVKLGELFHDLPKAVLAA 426 Query: 1308 LIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQ 1487 +I VNLK L+QL+D LW+ ++ D IW+V+F ++ L+L G+ V V FS+L+VV + IIIVNLKGMLRQLSDMRSLWKANRADLLIWLVTFTATILLNLDLGLVVAVIFSLLLVVVR 486 Sbict: 427 Query: 1488 TQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLYFANSEIF------ 1637 L QV DTDIY + Y+ A++++G+K+ + +YFAN+E + TQMPHYSVLGQVPDTDIYRDVAEYSEAKEVRGVKVFRSSATVYFANAEFYSDALKQRCGV 546 Sbict: 487 Query: 1638 ------RQKVIAK--TVSLQELQQDFE-NAPPTDPNNNQTPAN-GTSVSYI----- 1760 ++K++ K + L++LQ++ + P N TS+ +
Sbjct: 547 DVDFLISQKKKLLKKQEQLKLKQLQKEEKLRKQAASPKGASVSINVNTSLEDMRSNNVED 606 Query: 1761 -----TFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGI 1925 A + ++AP + S + A P FH+LILD+ +SFVD + +SD Sbjct: 607 CKMMQVSSGDKMEDATANGQEDSKAP-DGSTLKALGLPQPDFHSLILDLGALSFVDTVCL 665

Query: 1926 KALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAVLFAQAN 2105

K+L + + +I V+V++ H+ V + + G F D S+ KH+F S+HDAV FA + KSLKNIFHDFREIEVEVYMAACHSPVVSQLEAGHFF-DASITKKHLFASVHDAVTFALQH 724

Query: 2106 ARDV 2117 R V

Sbjct: 725 PRPV 728 (SEQ ID NO :4)

Hmmer search results (Pfam):

Model Description Score

PF00916 Sulfate transporter family 254.5

PF00189 Ribosomal protein S3, C-terminal domain. 3.3



Docket No.: CL000861 Serial No.: 09/749,589 Inventors: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER...

Parsed for domains:

Model	Domain	seq-f	seq-t	 hmm-f	hmm-t		score	<u>E-value</u>
PF00916	1/1	187	497	 1	328		254.5	1.5e-72
PF00189	1/1	651	661	 79	89	.]	3.3	8

JAN 1 5 2003

R TO SMALL

Docket No.: CL000861 Serial No.: 09/749,589 Inventors: Karl GUEGLER et al. Title: ISOLATED HUMAN TRANSPORTER...

1 CTGGGTTCCT ATGTGGGGAG GTCATGCTCC CCACTCATTG AGCCCCCCCA 51 GGCAAACCAC CTGGACAGCC AGACCCATGC AGACTCTGGA GCAGGTGGAG 101 AGGAAGAGTG AGACCACCCC GCCTCACGGG CGGTGAAGGG CCGGCAGCCT 151 CTGAATAGTC TCTGCTAGGA GGTAGAAAGC ACCCTCCCAT CTTAATCATA 201 GTAATCATCG CCACTACCAT TTACTGGGTG CCTATAAAAG GCCAGCCTCT 251 TCATACACAT GATCTCACTG AATCCTCATA GCATCTGCCT GCGACTGTTA 301 TTATCCCCAT TTACAGATGA AGAAACTGAA TCTTTGAACC CAGGTCATCT 351 GGCTCTCAAA CTTGTGCTGT TTTCCCTAAG CCACCCGGTC TCTCATTTCT 401 CCCACTGAAA TGTCTCACAT GCCATTGCCC TTACTCATTT CTGCCCATGT 451 CTCCTCCAAA ACACCATTTA TCAATTCGCT CAACAAGTAT GTGTTGAGTA 501 CACACTAAGG GCCAGGCGAG GGGCTGGGCA CAGGCGCTGG GGGTAGGTTC 551 ATTCTCCCAC CTTCGCTTCT GCTGGGTATC ACCTGTGGGG TCTTGCCGGG 601 CATCCCACCC TCACCTGTAG TTCAAGTGGA CCTTGGGATC CCAAGACCAA 651 ATGAATGGAA TGCACCAGCC CAGCCTTCAC CAACTTGAGC ACAATCTTAT
701 TCATAATAGA AACTCACATT TGCATCACAC TTTACATTTT ACACAACCCC
751 TTCTTATCCA TTAACTCATT TGATCTTCAC AACAACCCTG TGAGATATGT 801 CTGTTACTCC CACTTTAGTG ATACAGAATC TGAGGTTTGA AAAGTAATGC 851 TGACCATTCT GCCTCATTAA TAAAAGCAGG ATTAACCCAG GCTCCTGGAC 901 CCTTCCACAA AAGGCATTAA GCAACCTGCT CCCCTCTGAC AACCTCCCCT 951 GTCACCCAGG CTCTCCTCTG GGAAGTTGGG GGCATCTCTA GCCCCCAAGT 1001 AGTTACTCAT TITCAACCCC ATCTCAAATC TITTGCCAAA CTGGCCACAG
1051 CCACCCCACA CTCCCCACCT CCCAGATACA AATCCTCACT CTAAGCCTTC
1101 CCCATCTCTT TCTTCTCTGT CCTTCTTTCT CTGTGGTCCT CTGAGCAACT 1151 TCTCCCAGCT CTGGGAGGTA GAGGGGAGGT GGGAGACCCA GTAATTGGAA 1201 GAGGGAGGGG GAAAGGTTCC TACAGGGAAC TCCTCCGGGC CTCAGGGGCC 1251 CTGGCACTCA GCTCTGCCCA TCTCAGCTCC TGGAACGTCA GCCAGGTTGC 1301 GCAAAAAGTG AGGAGGAGAG GAGCGGCAGT ACACAAGGGT GGGGGAAAGA 1351 TTAGGCACAG GAAGCCGTGG GAGAGAGAGC CGGCAGGTGG ACCATCCTGG 1401 TTTCCCCACA CACACCATTG TCCCCCTGGG AAACCTGTTG GTGAAGTTCT 1451 AGATGTCTTA TCCAAGAAGG GTCCTCTTGA GGTCATCTCA GCTATCCCCC 1501 TGCCTCTAGG CAAGCTGTTT TCTGTTTCTT CCAAGCTGAC TGGCTGAATG 1551 GTAGGAGCCT TTCTGCCAGG GAAACTAAGG TCTGGGAAGG GAGTATGGCT 1601 TGTGGGGACA CCAGGGGTCA GGGGAGGGGA GGGTCCACCT GCTGAATCAA 1651 GTGGGGCCTC CTGCCCTCGT GATTCCCCTT TGCCTGGTGC TCAGTGGGGG 1701 TGATGGTGAC GCCACAGGTG TGGAGTGCCA GCCACGTGCT GAGCGCCAAG 1751 CAAAACAGCC AGGGTGAGTC TATGCATCAT CAGTGCCTGG GAAGGAAGGC 1801 CACTGCGAGC AGGGAGTCTG ACGGAAAAAC TTGACAGAGG GAAGGGAGGC 1851 ACCTTGCTTT ATCGGGCGG GGAAGGCCAG AATAAAACTC TGCTACTGCA
1901 AGGACCAGAG AGAGAAGGCC TGGGCTGGCA CTAGGGAGGG ATGTTCCCTC
1951 ACCCTCCCCT CCTCTGCTTC TCCCAAAGGCT TGTAAATGCC CCAGATATGA 2001 GCCAGCCCAG GCCCCGCTAC GTGGTAGACA GAGCCGCATA CTCCCTTACC 2051 CTCTTCGACG ATGAGTTTGA GAAGAAGGAC CGGACATACC CAGTGGGAGA 2101 GAAACTTCGC AATGCCTTCA GGTAACTGGT CCAGAGCCCA GACTTCTGCC 2151 TCCTCTGCTC CCTACCAAAA TCCTTTCTGC ACCAGGACAC GGCTTCTGCA 2201 CTGGTATCCC TAAGATGGGG TTAAGGGAAG CCCTGGGGAA GTGAGGTTCT 2251 GAATGATGAA TTTAAGATCC TACAACCTCA TCTGTACTGA GACCCCCAGG 2301 GAGGATGGGG AGCAGGAGCA AGAACCATCC AGAAGGGTTA TATGGCATTC 2351 CCAAACCCCT GCATGGCATC TCCCATATTC TCAATTCACC CGGGTCTCTC 2401 TGGGTTTGTT AAGGCATGGT AGATGAGCAT CTACGTTATG GAGGGGTGGG 2451 GAGCATCAGA GCCCTTACTC CATGCCCTGT TCCCTCCTTA CAAAAAATAC 2501 CTGAAGTTAC CATCACCCCA GGTTCTTTGT CCTTTCCCTC CCGGATGTTC 2551 CTTCCTCCAC TTGGTCCAGA GAATGCCAAA AGGAGGCCCT AAATTTCTGA 2601 ACTITCCTGA GGGGACCTAC CAGGGTGTAG TCCTACCAGC GCCCAGGGTC 2651 TTTCCACTCT CATCTCCCTG GAAATGCGAT GGTGGGTATG AAACCTTGTC 2701 CCTAAGTAGG CGCTACACAA GGTGATCCAT ACCCACACCC CAGGAGGCTG 2751 GGGCTGCGGG TGTCACCCTC CCCATTCCCA GACTCCTGGC AGACCTCCTC 2801 TGGCCCAGCT ATAGGCCAAC TCACTCTCCC TCACTCCCTT GGGGAAACGG 2851 CTGATTCAGT TACCTGGATT GAGGTCACTG GCAATGGCTG AAGTGGAGAC 2901 GCAGGTGGAA CTGGTTCAGG CCGGGGGAAT CACCCACTTG AGTTTGTACT 2951 AAAAGCCCCA GCCCAGCCCT GTTTCTCTTG GGAGGCTCCA TTTCTGCCCA 3001 GTTACAGTCT GTCCTCACAG CTGTGCTCCT CAGACAGGTG GTCTCTGCCA 3051 GTCTTTGTGC CCAAGACTTT AGGGCACAAA GTCTGAGGAT GAGAAGATCT 3101 GCTATTGTCC TAAAAGATTA GGATAATGAA AGCTGTAAAG GGATATAGCA 3151 AACTAACAAT TCCTATGATA CTGGCATGAG AGCCTTGAAC AGTGCCTGGC 3201 ATAGAGAAGG TGCACCAATA AATATTTGTT TCATGAATGA ATGAATGAAT 3251 GAATGTCTAG AAAGCTAATC CCTCTCAGCC TCTGTTTCCA GTTCTTCTTT 3301 CAAGCTTCAG ATTGCTTTGC CCAACATACA GCAGACTTGC AAGTAAGGTT 3351 GGGCATGGAC TAGCCCTCAA ATGAGTTGTT TTTCTTTCCC TAGCCAGCTC

JAN. 3401 TCTATTCATA AGTCCGGCTT TCTCTGCCAC AAACAGACCT GATGGAGCCC 3451 CTGCAGGGCT GGTTCTCTCT TCAAGCAAGG CTTTAGAGTT GCATTAAGCA 3501 ATTTATCCCC CGTCCACCTC CCCTTCCAGC ATCCCAGGGA TGGCAGAGGC 3551 ACCCATGAGC CCCAGAAGGG ACAGGGGGTA AGATATTGAT GATGATGCTT 3601 TTTCTTGGAG TGTTAGTTGG AAGAGAAAAT CTGCCCAGAC TTTCCAAGGT 3651 ACAAAGCATT GTCTTTGTTG GTTTCAGTCT TGGGTGACAT CCAGGGGACC 3701 GAGTGTCAGG GAAACTATTG TTGAGCAAGA GCAAAGAGCA GGAATTGGTG 3751 CTGGGCAGGA AAGGAAGCCT CATCAGAGCA GGCCAGTGAG TCACCAAATG 3801 GGCCCTAAGT ATTTGAGTTC CCTCAACTGG GAGAAGGAAA GCAAATGCCC 3851 CTCACCCACT TCCAGTCATC AATCCACCGG CTGTCACCCT TGAGTTTGTA 3901 AGCCCTTGTT CCTACCGCTC CTGAGTTTCT ATGAAAGGAC CTTGAGGTGT 3951 TCAACAAACA GGGAAGGGAT CAACTCTCCC CACCCTGCGT TGACCAATGA 4001 ATTCTTCCCT CCTCTGCTGC CCAGTGAATT AACAGGAGAA AGAACTCCGG 4051 TATTGGAGTT ACCACACATA AAGGATAGTG AGTCAGCAGA GTGCACCCTG 4101 CAGGAACAAT AGAGCCTTCC TTTTCAAGGA AGTTCTAAGA AAAATGGCAG 4151 CAGGCAGGCC CCACTCGGGT GTATTCACTC ATTCATTAT TCAACAAATA 4201 TTTACTAAGT GCCCCTGTGC AAGGCTCGAG GTGTACAAAG ATGAACAGGA 4251 GAGCTAGACT TCTTGCCATG CGTGGTGGGG TTTGCTGCCT AGTGGGAGAG 4301 ACAGACAAAA AGCAAGGAAT GCACACAG GATGCACACA CAGCGGCAGG 4351 AACCAAGGTG CAGTTACCCA GGCCTGGGAT CAGACAGACA GGACTCAGAG 4401 GAGACTTTCC CAGAGAAAAG CCATCTGAGC CAAGGGATGG ATCTGATACC 4451 TCCGAAGGCT GAGCCACCAT AACACTCATA CCTTTAAGCC AAGTCTTATA
4501 AACTCCCCAG GTAAGCAGCT GGCAGTCAGA AGACCTCCAG CTAATGCCCA 4551 GGACAAGTTG ATGAGCTCTC AAGAAAAAGT TCCTGCCTTT TCTTCTCAAT 4601 ATCCCTGGCA CACAGTTCAG TGAATTTTGA ATGAACCAAT GAATGAAATG
4651 AGCAGGATAT GATAATCCCT CTCCAACACG GAATGTCCAA GCCATGCAGA 4701 GCCGACTGGA AATTITCCCC GTTCCCTTCC AGATGTTCCT CAGCCAAGAT 4751 CAAAGCTGTG GTGTTTGGGC TGCTGCCTGT GCTCTCCTGG CTCCCCAAGT 4801 ACAAGATTAA AGACTACATC ATTCCTGACC TGCTCGGTGG ACTCAGCGGG 4851 GGATCCATCC AGGTCCCACA AGGTGAAGGG GCTCCTTCAG CCAGGCCTGG 4901 ATTGCCACTC CCCTCACCAT TCCTCTCCTC ATCCCCACTC CATCCCTCTG 4951 TGATCCCCAT AAGCTAGTCA TGCTGCTGAG CTTCAGTCTC GTTGTCCTCT 5001 GCAGGCATGG CATTTGCTCT GCTGGCCAAC CTTCCTGCAG TCAATGGCCT 5051 CTACTCCTCC TTCTTCCCCC TCCTGACCTA CTTCTTCCTG GGGGGTGTTC 5101 ACCAGATGGT GCCAGGTAAG GCCTCTCCCC TCTGGGCAGG CAGGATGACC 5151 CAGACCACAA GGATGGGAGG TGTGGCAAAG GGGCCTCGGG AGATTTTCCA 5201 TCTGCATTCT CCTGGAGTTG TTCCTGGTCA GTCCTAGGGG AATGGTCACT 5251 GTGAATGTCA TTTCCAGGTC CTCGGTGACC TTGGAGAAAC CACTGAGCCT 5301 CTTTGAGTTC AGTTAGCATT ACCTGTTCCA TCTTCCTCCT AGGAATGAGA 5351 GGAAGACTTA GCAGAACAAG ATATACCATA TGCTATAACA TGCTTAAACA 5401 GATGTGAGAA ATCACCATCT AACTCCCTGG TTGGTCCCAG CCGGCCACTA 5451 CAGGGACATT TGGACTTCTC TGGTGCTAAG TGAGATGGAG GAAAGCCTGG 5501 TCACAAGGGC TGGTTTCTGG TTCAGGCTCT GCTTATATTT CTTATTTCTG 5551 AGTTCATTTT CTCACGTGTC CTGTATGACA ATATTGACCA TTGGGGTAAA 5601 AGCACCTTGA AAAGCATAGA TCATGGTTAG AGTGAGTGGT TGTTATTATT 5651 GTGTTGGAGA AGAGCCTTGG AGGTGCAGGG ATCCATCCCC CTGGGGTCGG 5701 GAAGCATTCC TGGGCCCCTT TCTGGTTTCC ATCGGTGTGG TTCAAACCTC 5751 TGATTTTGC TGGCTGGGTG GGGCACCACA GGTACCTTTG CCGTTATCAG 5801 CATCCTGGTG GGTAACATCT GTCTGCAGCT GGCCCCAGAG TCGAAATTCC 5851 AGGTCTTCAA CAATGCCACC AATGAGAGCT ATGTGGACAC AGCAGCCATG 5901 GAGGCTGAGA GGCTGCACGT GTCAGCTACG CTAGCCTGCC TCACTGCCAT
5951 CATCCAGGTG AGGGGGCAGC CCCCAACCCT GCTAGAAGGG CATCAGACCA
6001 CCCTGCCCCT CCCTCAAAGC CTTAGCTTTG ATGCTAAATC TGATTTAGGG 6051 GGCTGGGTGT GGAGGCTCAT GCCTGTAATC CCAGCACTTT GGGAGGCTGA 6101 GGAGGGTGGA TCACTTGAGG TCAGGAGTTT GAGACCACCT TGACCAACGT 6151 GATGAAACCC CATCTCTACC AAAAATACAA AAATAATCCA GGCTTGGTAG 6201 TATGCGCCTG TAGTCCCACC TACTCAGGAG GCTGAGGCAG GAGAATCACT 6401 GGCTAAAGTG AACCTTGAAA ATTAACAGTA TCTCCTCATC TGCATGTAGC 6451 AGGACCATAC AAAAAAACAA CAGCTGTACC TGGTTAAACT GTCCTGAGCT 6501 TTAAACCTGT AAAAGACTCA CAGCCTCTCT CCATTATCCC GTGGAGAAAC 6551 CCAACTCTCT GCCAGCATAG TCTTGCAGAC TGCTAATTTT CTCTAACATC 6601 CCTCACTCCG CTCCAGCCTC CTCTGCTCCA AGCCACAGCA GCAGTTGCAC 6651 AACATAAATT GAGCTTCTGC AAATGGTTGC AAAGGATTCT GCTAGGTTTT 6701 ATGAAGGGAA GCACAACATG ACAGAATGCA AGAGCAAAAC ACAGTCCCAG 6751 AGAGCGCCTT TTCATTCACT CATTCATTCG GTTTTGTGCC AAGAACTAGG

Docket No.: CL000861
Serial No.: 09/749,589
Inventors: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER...

6801 CTAAACCCTG GGATACAAAG ATAAGTAAGA AAGAGGTCCA ATTCACAAGT 6851 TGCTCACAGC CCAGCAGAGG AAGGAGCCAT GTCAACAGAT AAATTTGTAT 6901 GCAGTGAGAT AAGCAGCAAA GTAGAGCCAT GTACAAAGAC TGTAGGGACA 6951 CAGAGCAGAG TCACGGAGGA CCTCAAAGAG GAGGTGACAC TCCACCTCTC 7001 TTAAAGGATG AGAACTTAAC CAGGAACAAG GTATACAGAG GATGGTCCAG 7051 GCAGAAGGGA ACAGTGCCTA AAAACACTGA GGCCTGAGAG AGTGTGATCT 7101 GCGCAGGCAA AGTAAGGGGC TTGGTGTGGC TGGAGGGTAG AGGGCCCAGA 7151 AGAGGATGGA AAAGTAGGCA GGAGCCAGAC AATGAGATCT GGGGTCTGTT 7201 CTCTGACAGC GACTTTGGGT CTGATTGGCA GTTTATAAGG ATCGTTTGGG 7251 CTACACAATG ATGAGTGGGA GGTGGATTAG AATCAAGGCA GGGGACCTGT 7301 TGGGAGACTC TGCAGAGGCC CAGGCAGGAA TAATGCAGGC GAAGACCAGG 7351 TAGAGAAAGA GATGGGGCTG GACTTGAAAA GAATGTTTTA CCAGGAGCTT 7401 GGTGATAGAC TGGATGTGGG AGGTAAGGGA GGATGACTCT CAAGTTTTTG 7451 GTTGGGCAAC CAGGTTAATG ATGGTGTCAT TTACTGAGAG AGAAAACACT 7501 GGGGGAGGAC TAGACTTATT TTACAGATAA GCCAAAGCCA GAGAGGTGAT 7551 GTGACAGAAA GGCCCATGCT CTAAAGGAGC TGAAGGTCTG ATGGCAGCCA 7601 TGTAGAGCAC AGTGAAGGGC AGGTGAAGGT CACAGATGGT CCAATTCCCT 7651 CAAGCTACTG CTACGCTAGG ACTGCACGGA GCTCCAGACC TGCGTGTGTG 7701 TGGGGCGGGT CGTTGGAACT GCTGAACCAC ATTGGTCTTC CGCCACCAAC 7751 CACCCTTTTC CTCCTCTCAG ATGGGTCTGG GCTTCATGCA GTTTGGCTTT 7801 GTGGCCATCT ACCTCTCCGA GTCCTTCATC CGGGGCTTCA TGACGGCCGC 7851 CGGCCTGCAG ATCCTGATTT CGGTGCTCAA GTACATCTTC GGACTGACCA 7901 TCCCCTCCTA CACAGGCCCA GGGTCCATCG TCTTTGTGAG TCTGGGGATG 7951 CACCCCTGCC ATTGGAGCAA GGCTCCAGCA GACACATGAG GAGGATGTAC 8001 TGTTTTAAGA TGTCGTGAGC TCCTCATTGC AAGGGCTGGC TTAGCTGTTG 8051 TTCAGAGAGG ATTCTGAGGG GGTTTCTGTC TTGGGAGGGT CAAAGTCATG 8101 ACTCACAGAG GTTCTTGGTA GTTAATACCT GCAGAAAAGA GCTGTACATT 8151 CTCCGCCAGT TCCCCATTCT AGTGCCTCAA CCCCTCCCTG CCTGGAAAGT 8201 CCTGCCTTAT GTCTAATCTC CATCCCTCCT CCTTCAGCCC AAACTCTTCT 8251 AAAGAAAAAG AAAGCATTCC TTTTCTAGCA CAAGTTCCCC ATGTGCCTTT 8301 TGGGAAAGGG CGGTGGGCGA CGGGACAGGG TTCCTGATCA GGGTTTTAAT 8351 TCTGTCTTGG TGTGCCTCCA TTAGCTTTGA TGGCATCCCT TCCCTGGGTC 8401 AGACACCCAA AGGTGGGGTA TTATGGGAAG AAGGGGTGGG AGCCTGTGAG 8451 CATGATGCTC TTTCCCCCAG ACCTTCATTG ACATTTGCAA AAACCTCCCC 8501 CACACCAACA TCGCCTCGCT CATCTTCGCT CTCATCAGCG GTGCCTTCCT 8551 GGTGCTGGTG AAGGAGCTCA ATGCTCGCTA CATGCACAAG ATTCGCTTCC 8601 CCATCCCTAC AGAGATGATT GTGGTAAGGA CCTTGTTCAG AGCTGGGATG 8651 TTGGGGGGCC AGGCTGTGAG ACGAGGAAGC CCCTACCTTT CCTCACCCCA 8701 TCCCCTCAAC TGGCAGCCAG TGGGACAGGA AGTCAGTTGT GAATCCATCC 8751 CATCCCCCGT ATGTGGCGTT TCCTCTCTTT CTACTGCTCT AATAATTCCC 8801 CCTAAGGAGG CAGGGGAGTG GGATTCAGGG TCCCCAGAGA AAAGGGAGAC 8851 TTGAGAGAGA CGCCTGCCCT GGCCCCACCT TAGGGCCAAT CCCCATTCTC 8901 CACTCTGGGG TTTGCAGGTG GTGGTGGCAA CAGCTATCTC CGGGGGCTGT 8951 AAGATGCCCA AAAAGTATCA CATGCAGATC GTGGGAGAAA TCCAACGCGG 9001 GTGAGTCCAG GTGGCCCAGA AGCCTGGCCC ACCCGCACCT CATGCCCCAC 9051 TAAGGCCTGA GCTCGGAGAG GGAGACAAGA TGAACTCTAT GAAAGTGCAG 9101 TCGAAACTGT ATGACACTGA CCATGTATGA ATTATTACTA TTACCGTTTC 9151 CTGAGAAGGG CCGCACAACC AGCCAATGTA GGCTATTTTA TGAGAAATGA 9201 GTCTTAACTG CCACACTCCC CTTATAAATC TCATTCAACT GATGCTGTTA 9251 AACAAAGCCT CTCTGAACAG CCGCTTGCTG GCTCTTTGCC TTGCTCTAAT 9301 GCATTGGTTC TTTGTCCATG TAGAAAGGGA ACTATTAGGT TCAACCAGAT 9351 TCATGAAGCA TCCACTCTGT GCCAGGCACC ATGCTGGGCC CTGGGAGGAG 9401 AGGGGTGACG CTTGTCCTGC AGGGTTGGAA CAGGCAAGGG AGGGAAGACC 9451 ACATAGCACC AAAGGTCTAG GGGTCTGTGG ACTCGTGAGC ATACAGGGTT 9501 CAGAATCTGG GAGTTAACAA ACGAGGCCCT ACCACATACT GGCCCGGGGA 9551 CCTTGGGCAA GTTAGGTTCT CTCAGCCTCA GTTTCCTCCT TTGTAAAACA 9601 GGAGTGATGG TCCCTACCCT ATGGGGTGGT GCTGAGGATT CAGACTGGAT 9651 GGGATAACTT AGGCAAAGAT CCCGGCACAC CATGGGGGCC TGGCTGGTCC
9701 CTGTGGGCTG GTGAAGGACT TGGCTGCCCT CCCCACTCAC ACCCTTGGGT
9751 TCTGCCTCCT TCCTGGCTCC TCGGCAGGTT CCCCACCCCG GTGTCGCCTG 9801 TGGTCTCACA GTGGAAGGAC ATGATAGGCA CAGCCTTCTC CCTAGCCATC 9851 GTGAGCTACG TCATCAACCT GGCTATGGGC CGGACCCTGG CCAACAAGCA 9901 CGGCTACGAC GTGGATTCGA ACCAGGTAGC TCTGGCCACC CCCGGCAGGA 9951 CTGGGCAGGA CAGGTCAACT CAGGCCTGGC ATGACATATC TTGGGTGGGG 10001 AGATCATTGG GCTGAGGTGA GGCAGGCTGC CTCGAGTGTG GGGGATAGGG 10051 GGTCCTCTGA CCCTAAGAGG CTGACCTCCT CTTGACTGGG AATGTGTGAC 10101 TTTATAGCCA CTGGGTCACT CTCAGGTCTT AGGCCCACAG TCCAGCTTGC 10151 ATGCCTGACT GCACTTGGTC CCCGTGCCCC CCAGCCCCAC ACTGGCTTCT

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10201 AATCCTGTCC CCTCCCTGCA GGAGATGATC GCTCTCGGCT GCAGCAACTT 10251 CTTTGGCTCC TTCTTTAAAA TTCATGTCAT TTGCTGTGCG CTTTCTGTCA 10301 CTCTGGCTGT GGATGGAGCT GGAGGAAAAT CCCAGGTGAG CCTTGTTCTA 10351 GGGGAGTTGG GGGGAGGTGG TAAGAGAACA GTTGCCCCAA AAAAGCCTGG
10401 GCACTGCAAG CCAGGCCAGC TCTTCTCCGA CCCCTTCTTC CCGTACTTAG
10451 TCTCCACTCC ACCAAAGCCA TGGATTGGAA ATAAATCAAG AGCAAAAATT 10501 TCACACCTTC CCTCTATCCC CAACTCTTTC TCGGAATAGG TGGCCAGCCT 10551 GTGTGTCT CTGGTGGTGA TGATCACCAT GCTGGTCCTG GGGATCTATC 10601 TGTATCCTCT CCCTAAGGTA AGAGCCCAGC CATCGAGCAG AAGTCAACGA 10651 AAGACTCCAA TAAGAACAAT CCCTGAGAGT TGTGTGGCAC TTTACGGACC 10701 ACAAAGTGCC ACTGTTGTCA TACTTAGTCT CAACCACAAA CTGTGAGGTA 10751 GACAATGCAG GTTTTATCCT CCCCATTTTA CAGGTGAAGG AAACTGAGTC 10801 TGAGAGTCTA AGTAACCTTG TCCATAGTGA GGCAGCTTAC AGCGCAGGGC 10851 TGGTCCCAAA CTCCAGCCTT CTGGCCTCAG AGTCTAATCC CTAGGCAACA 10901 TTTGCACCTA CCCACGAGTA CCAGGCTCTT ATATAGCCCA GCTAGGAGGG 10951 CTCTAGGCAT GCGTCATTTA GAGATGAGGG AAGAGAGATA GGGAAAGGAT 11001 GGGGCCAGGA AGGACCCCAT GGCTCTAACG CCAGCACTTT CCAAACCTAA 11051 GGTCGAATGC AGAGATTTGG GGGTCTAACG CCAGCACTTT CCAAACCTAA
11051 GGTCGAATGC AGAGATTTGG GGGATCAGC AGGGGAGGTG TTCCAGAACT
11101 CCGTCTCTGT CCTGCCAGGC CTTGGGGTCG GGTATGCGCA GGAGGGCAAA
11151 AAGAAGGGGA GACCCTGGGG TCCTGGAGCA ATGTTCTGCT TCTCTAGTCT
11201 GTGCTAGGAG CCCTGATCGC TGTCAATCTC AAGAACTCCC TCAAGCAACT
11251 CACCGACCCC TACTACCTGT GGAGGAAGAG CAAGCTGGAC TGTGTAAGTA
11301 TCGGGCAGCC TCTGGGTACT GGCCATGCCC CTGCCCTCTC CTCCAACCCC
11351 ACAGCCCTGT CAGCCCTGTC CTAACAATGA ACCCTCTAGT CTGCTGCTTC 11401 CTAATTAGCA TGAGATGAGT GGTTAAAAGT CCGAGTTTCG AAGTGAAACA 11451 TCCTATGTTC AAACCCTAAC TCAGCCATCT GCTGGCTCCA TGGCCAATAG 11501 CAAGCCCCTT AACCTTTCCC AGTCTTGGTG TCTTAACTGG GCAAATGGTT 11551 ATTTTATGCT CTCTGCCTCC CAGGGTTTTC TATGAAGAAG AAGCAAGGTA
11601 ATACAAGTAA ACATGTTGTC TACATCGTAT TTTATACTCA ATAAAGCTTA
11651 GCTATGACTA CTTTATGACA TACAGCTTTA AAAAACAAAA GGAAATAGTT 11701 TGTATTTTAA AAAAAAACCT AGAACATAAA GCCAGAGGAC CAAAATCTTG
11751 AGCAAGTTAC TAGACTTCCC TGGGGTTCTA TTTCCTCATC TGTAAATGGG
11801 GGTGAGACTC ATGCAGTCAT GGTTGCGTCA AACGCTGGTT CCGAGGATTA 11851 AATGAGATCC CAGTGGGAAA ACACCGCATG AGCGCAAACA TTCTGCAAAC 11901 ATGACTTATT GTCCTGATTA GTCACACACT CCACCGCATC ATCCGCTGGG 11951 CATAGTAATG AAGGCCAGTG TGTTTTGACG ACACTGCCTT CTCTCCATTT 12001 AAGCCCCACC ATAACCTATG GGAGAGGATT TACTAAACTT TCTTAACGGT 12051 GATGAAACCA AGGCTCAGAA TGGTTAAGTA AATTGTCAAA GGCCACAGAG 12101 GTAGGGAGTG GTAGAGTCTG GATTAAAACT CCAAGTCCTG GACTCCAGAC 12151 CTCTAGGCTG TACTGTCTCA TAGGGAAGGC AGTCTCACCC ACCTAGGGCA 12201 GAGAAGAAAA TCCTTAAAGC CAGAGAAGTG AGTGGCTCAT CTGTGGTCAC 12251 CCAGAGAGAC AGTGATGAGG ACAGGGAGAA AAATTATACC TCAGTTCCCA 12301 GCCCAAGGAT CTGCTTTGAC CATAACCCAA CAAGCCCCCG CTATGGTGGT 12351 ATTTCCTTAG GTTCATATGG CGGCTTTTGT TTCCATTTGA TCTTCACAGC 12401 AATTCTCTAC AGGAATCTGG GCAGATTTAT TTCCTTTAGA GGAATTTCCA 12451 GGTCTTAAAA TCTATAGGGG GCAACTATCA AAACTTCACC CAATGTTGCC 12501 CCCTACCCAC ACACAAAACC AGGCCCCCAG CCGATCAGAA AGCACTGCTG 12551 AGCTCCTGTC AGGGCCCACG CAGCTCGCTG TGAGACAGAG AGAGGGAACT 12601 CACATTTATT GATCACCTAC TGAGCATCCA TCACTAGGCT AGGACCGTCA 12651 CATTCCTTAA CTTTTGAATC CTTTCATGAG GTAGGCATTA TTATTCTCCT 12701 TTTGTTTCAC ATAGCCATTA AAGAACAAAA TTTGGGGCTG GGTGTGCTGA 12751 CTCACACCTG TGATCTAGCA CTTTAGGGGG CTGAGGCAGG AGGATCGCTT
12801 GAAGTCAGGA TTTCAAGGTC AGCTTGGGCA GCTTAGCGAG AGCCGTCTCT
12851 AGAAAAATAT AAAAGTTAGC TGGGTGTGGT GGCACGTGCC TATAGTCCTA
12901 ACTATTCAGG AAGGTTAGGC GGGAGCACAA CTTGGGTTCC AGGGTTTGAG
12951 GCTCCAGTGA GCTGATCTTG CCACTGCACT ACAGCCTGAG CAACAGAGCA 13001 AGACCCTGTG ACTCCAAAAA CAAACAAACA AACACATTTT GAACCCAAAC 13051 AGATCTGACC CAAGATGCAT GCTCTTATAG ATGCCACCTC CCTGTGTGCT 13101 GGGGCTTCTA CTAAAAACAC AGACAAGATC AGGCAACCAC AGTCAATCTA 13151 AGGGAAAGAG GAAAGTGTAA CCAAAGCACA AATACATAAA ATATTGCAAA 13201 AATGCTATTT AAAGAAAAAA AAGAGAAGAG AGGCTCTGAG GTTGTACTAA 13251 CAGAGAATGG CCTTGGCTAA TCCAGGAAGA CTTCCTGAAA GAGGTTGTTT
13301 TTTCCCCAGG TCTGCTTTTG ACATCTCTCT TTTCACAGTG CATCTGGGTA
13351 GTGAGCTTCC TCTCCTCCTT CTTCCTCAGC CTGCCCTATG GTGTGGCAGT
13401 GGGTGTCGCC TTCTCCGTCC TGGTCGTGGT CTTCCAGACT CAGTTGTAAG 13451 TGATAGCTTC CGCCCTCCTA GGCCCACAGT CGGTTCCCTG GGCCAGCCCG
13501 CAAAGGGCTT CCATGCCACG GCCTGGCTTA GTCCACTGTA CCTTCCACCT 13551 CTGGGCCTGG CACTGGAGGT GCTGCCAGGC CCAAAGAGAG CCCAACCCAG

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13601 CCAGGACTGT GGGCACAGTC TGGGCTGTTT GACTTCCCAT ATCTTGAAAA 13651 CCCCAGAGAA AGCCAGCATA CTCTTGCTGG GGATGGCTGG GGAGAGGGCA 13701 GTGGCAGAGA AAGGAGGGCA AGGGCAGGTG GTGAGATTCA ACATCCTTCC 13751 AAAGACATTG CCAGAACCCC AAACCAAATG GGACCCCACC CCAGGAGAGC 13751 AAAGACATTG CCAGAACCCC AAACCAAATG GGACCCCACC CCAGGAGAGC
13801 GCCAGGGTGG AAGACAGAAG CTGTGTTCTA CACACTGGAG GTATTACAGA
13851 GAAGGGGTCT TGGCCAAGGC AGGAGTACG CTGAATGTTG GGGGAATCCT
13901 ATCTTCTCTT ¢TTGAGAACT CAGAACAAGG AAATGATGAC TTCAGGGCGA
13951 CTCCCACCAC TTCTCCCACC ACTTCTCCC CCTGCCCTGT GGTCTGGGAG
14001 CTATGTCAAG GACCTGCCTG TCATCCTCAT AGTTATAGGA GGCCACAGGC
14051 CACCAGACAT GTGTCTCCAG TGCAAAAAGA CAGACACAGC AAGTCTGGGG
14101 GTGAGGACAG GACCCCATCC TACCTTGGCT CTGCCCCCGC CCCAGCAGGG
14151 GCACCCTTCC AGGCCCATGT GCCATTAGCA TTCTCTTATG TTTTTCTCTT
14201 CCTGCTTCAT CCAGTCGAAA TGGCTATGCA CTGGCCCAGG TCATGGACAC 14251 TGACATTTAT GTGAATCCCA AGACCTATAA TAGGGTAGGT AATTCAAGCT 14301 TATGACCTCC TTCTTTTGCT CTGCACCACC CCAAGAAGAG GTTGCTTTTT
14351 AAAGCCAATA AAGACATTTC TGCAACTTGA GCTCAGTCTC CCTGTCACAG
14401 GCCCAGGATA TCCAGGGGAT TAAAATCATC ACGTACTGCT CCCCTCTCTA 14451 CTTTGCCAAC TCAGAGATCT TCAGGCAAAA GGTCATCGCC AAGGTAAGGC 14501 TCAGTCCCTG GCGACCAGAG GCTCTGGACA GAGAGTGGCC GGAAAATGGA 14551 AGCAGAAGGG CGGTGGGAGC TGAGAATAGG CCACTCCCAT AGAGGGTGGA 14601 GGTCAAGATT GCTGTTGGCT CTCTCCCTGC AGACAGGCAT GGACCCCCAG 14651 AAAGTATTAC TAGCCAAGCA AAAATACCTC AAGAAGCAGG AGAAGCGGAG 14701 AATGAGGCCC ACACAACAGA GGAGGTCTCT ATTCATGAAA ACCAAGGTGA 14751 ATGAAGGCCA GAAGCAGCCC CGTGCCCTGC, TCTCCTGCCC ATTCTGATAC 14801 TGCCCCCTGT TACTCATGGT ACCCTGGGGG CCCCGCTTCC CACCCTGACA 14851 GGCAAAGACA GAAAGTCTCT GGGAACACTG CCTGGTGGCC GCTGGGCATT 14901 TTTCTTCTTT TTTTTCTTTT TCTTTTTAGA GATGGAATTT TGCTCTTGTC 14951 ACCCAGGCTT GAGTGCAATG GCGTTATCTT GGCTCACTGC AACCTCCACC 15001 TCTGGGGTTC AAGCGATTCT CCTGCCTTAG CCTCCCAAGT CGCTGAGATT 15051 ACAGGTGCCA CCACACCCAG CTAATTTTTG TATTTTTAGT AGATATTGGG 15101 TTTCACCATG TTGGCCAGGC TGGTGTCAAA CTCCTGACCT CAGGTGATCC 15151 ACCTACCTTA GCCTTCCAAA GTGCTGGGAT TACAAGCCTG AGCCACTGCG 15201 CCCAGCCTGG GCATTTTCT TCTTGGATGA GGTGCTACCA TCTCCCAGGG 15251 AAGCCACTGA ACCCCCAAGG CCCTTCTCCA TTTTCTGGCT AAGATAGGAC 15301 ATGGCCCATG GACTTTTGAA CAACCCAGAG GGGGAACAGC AGTGAATTTC
15351 CTGGGGAACC CAGGCAGCCC AGGGCTAGCA AGGCTGGGGT GGCCATGGCA
15401 GTAATCCTTG TAATCCCAGC ACTTTAGGAG GCCGAGATGG GAGAATCACT 15451 CTCATGAGTT CAGGAGTTCG AGACCAGCCT GCCCAACGTG GCGAAACGCT 15501 GTCTCTACTA AAAATACACA AAAATTAGCC AGGCGTGGTG GTGGGCACCT 15551 GTAATCCCAG CTACTCAGGA GGCTGAGGCA CGAGAATCAC TTGAACCCGG 15601 GAGGCAGAGG TTGCAGTGAG CCGAGATAGT GCCACTGCAC TCCAGCCTAG 15651 GCAACAGAGG GAGACTCTGT CTCAAGAAAT AAAGGAGCTC AGTGTCCCCG
15701 GAGGGGCTTT CTCCCAGAGA GAGTGGGCTT GAGGCTTCAG TGCCTCTCTT
15751 GGCTGGGTCC TCTGACTTTG TCTGGGTTGT AGGAGACCAA GTTTGCAGGC 15801 CCTGCCTAAG AAAGGGCTTT GGGAGAGGCC TCTCTGGTGG AGCTTTCAGG 15851 GTCTGTGTTC ACCATCACCG AGGCGAGTTA TTCCCCTACA CCTACACCCT 15901 CCATGCCCCT GCTTCAGTCA CAGCAAGGTC TGGCTCAGTC TGGTGGTCCC 15951 TGACTCTGCC CACTGTCCCC ACCCTTCCAG ACTGTCTCCC TGCAGGAGCT 16001 GCAGCAGGAC TTTGAGAATG CGCCCCCCAC CGACCCCAAC AACAACCAGA 16051 CCCCGGCTAA CGGCACCAGC GTGTCCTATA TCACCTTCAG CCCTGACAGC 16101 TCCTCACCTG CCCAGAGTGA GCCACCAGCC TCCGCTGAGG CCCCCGGCGA 16151 GCCCAGTGAC ATGCTGGCCA GCGTCCCACC CTTCGTCACC TTCCACACCC 16201 TCATCCTGGA CATGAGTGGA GTCAGCTTCG TGGACTTGAT GGGCATCAAG 16251 GCCCTGGCCA AGGTGAGGCC CTCGGGGACA GCAAGCACCA CCCACTCCAC 16301 CCCCTCCGCT CTGCTCTCCA CATTCCCTTT CCTGGGAGCC CTCATTTCAG
16351 GAAGCTGAGG GAGGAAGCTC ACTGGGGAGA CTAACAGCTC CTAGGAATCC
16401 CTCCTTTCCC CAGACGCCAC CAGGTTGAGA CATTCTCCAC AGAGCAGGCC 16451 CAGACGGCCC ATGACAATGA GTGGCGGGAC AAGTCTACCA GAGTTTCAGG 16501 CCCCTGTGCT CCCAACACCC CCAGCAGTGG CCATCCCAAG TCCCTCTCAG 16551 CCATCAGGAA CCCACCCAGG TTCTCTGAGG AGGGTCCAGT TTGGCTCCTG 16601 GTTCATGATC TGCTGCCCTT GTCCCTCATT CACCAGCCAC CCTAGGACAG 16651 GAGAAGAAAT AATACCAGTG CCCCACACCA TCAGGCCAAA CAGAGAGCCC 16701 ACGGGACACC TTGAATGAAT GTATCCATCT GATAACTTTC CAGCAGCCAC 16751 CGCCAATGGC GGGAGTCAGC AAACCTCAGA GCTGGCTCAG ATAGAGGCAA 16801 GCCAGGGGAA CAATGGGCAC AGAGAGTGTT CGGACTGCCT TCACCATCAA 16851 CCAGGCGCAG GGCAGGCCCC ATACCCAGCC TTGGGCCTCA GCCGGCTTCC 16901 TTAGCCAGGA TCTGGAGTCC AGGCCAGCCT TGGCTGAAGC TCTAGACTCC 16951 CTGAGCCTCC ATCCTCCCCT GCAGCTTCTG TCTGAAGCCA CAAAGAAGTC



17001 TGAGAATCTA AGCTACTGAA AGAAAAGATC AGCCGGGCGT GGTGGCTCAC 17051 TCCTGTAATC CCAGCACTTT GGGAGGCCAA GGCAGGTGGA TCACAAGGTC 17101 AGGAGTTCAA GACCAGCCTG GCCAACATGG TGAAACCCCG CCTCTACTAA 17151 AAATACAAAA ATTAGCCAGG TGTGGTGACG GGCCCCTGTA GTCCCAGCTA 17201 CTCGGTAGGC TGAGGCAGAG AATTGCTTGA ACCCAGGAGG CGGAGGTTGC 17251 AGTGAGCCAA GATCGCGCCA CTGCACTCCA GCCTGGGCAA CAGAGTGAAA 17301 CTCCATCTCA AAAGAAAAA AAAGAAAATA TCTAGCCCCA CAAGAAGGGG 17351 CCATGGTGAC TITAAGTGCC CGCCACGTTG GCAAAAGTCC ATTTCCGCTC
17401 CACTTCCCAG AGAAACCGTC AGCCAACACT CCAGGGAGAA GTGGTGTGCT
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17501 TTTGGCTTCC CCTCTGAAGT ACGTTTTGTG AATCACTTTT GAGACCCACT 17551 CAGAACATTC CTTTCCTTTT GCCTCCCTAC CCCAACAACA CTTCTAGCTG
17601 AGCTCCACCT ATGGGAAGAT CGGCGTGAAG GTCTTCTTGG TGAACATCCA
17651 TGGTAAGAGA AAGAGGACAT TTAGGGACTG AAAGACTGGC AAGGAGTGTG 17701 GGGTAGGAAC AGGTTGGTGG GGTCTGAATA GTGAGGAGGT TGGAAACGAG
17751 AGCACCCAGC TATCCCCCAC AAGCTGCTGC CTGCTCATAA AAGCTTCAGG
17801 TACAAGTCCA AAGAGACTGG TCAGATTGCA TAAACATCCT AGGGGCCTTA 17801 TACAAGTCCA AAGAGACTGG TCAGATTGCA TAAACATCCT AGGGGCCTTA 17851 GTGACAGAGT GGGGGTGAGG AGGTCATGGA GTTACAGAAG GACAGCTAGG 17901 ATTCTAATCT ACCCCATAAC TAATTTGCCA CGTATCCTTG GCCGAGTCAC 17951 TTTATCTCTC AAGGGATCCT TTTCTACCTA TGTAAAACGA GAGGGTTGAC 18001 TAGATGGATT TGGGGATCCT CTCCCAATCA GAAACTCTGT GAATCGATAT 18051 AGGCATAGAG CACACGGTAC CCTAATCCC CAGGGAACAT ATAAATATGC 18101 AGTTTTGTAG GCATACAGCC TCCAAAGGGT GCATATACAC AGCCTCAAGG 18151 ACGTGGCCAC AGGGCAGCAG ACATTTACAT GACTAGCATG TACGCAAAGT 18201 GCAGAGATGT GGGAGCAAGT GCACACAGAC ACACAGGGAA ATGTGAAGGG 18251 GCACATACAC ACACACCCAG CTCCCTGCAC TGGGTCAGAC CCCCCTCCAGC 18301 AGGGCTGCAG TCCCCAGC CCCCTGCAC TGGGTCAGAC CCCCCTCCAGC 18351 CAGTGGCAAT GACCTGCTAT GATATGTTCT GAGGTTAGAA GCAGTGGATT 18401 CTCCCCAACC TCACTGGACA CCCCCTTAGG AAACCATCTC TAGGATTAAG 18451 AGTAATCCAC ACAAACTTCC AATGCCACAC ATTGGAAGTT GCTGGAAAGG 18501 TCTGGGAAAA CAAGAGGAAG GATGGGTCCT TGGGGGATAG AACTGGCAGC 18501 TCTGGGAAAA CAAGAGGAAG GATGGGTCCT TGGGGGATAG AACTGGCAGC 18501 TCTGGGAAAA CAAGAGGAAG GATGGGTCCT TGGGGGATAG AACTGGCAGC
18551 GGCCTCTTCA AGGATGGCTT AGGCTTTTCC ACTCGAATCA CCACAAAGTA
18601 CTGACTCCCT AAATCAAACT GCTTCCTTCT GCTCTGGGTT GAAACTTCAG
18651 CATCCTCAAG TTCATGTTGC CCTCTGCCGT CCAGAACTGA TATTGCACTG
18701 CCAATGCCAT GGCCCTCAGA TACAGCAAGA GCTGGGACCT CAGGCCTCTC
18751 CCATCCCTGC TCTGGTCTCA CTATCTTCCC CACCCCCAGC TCCAATCCAC
18801 AATGGCTGTT ATCTTTCTGA AGGCTGTTT TTCTCCTTCT AGCCCAGGTG
18851 TACAATGACA TTAGCCACGA TACACCACGA GATCCTCTT GACGCACGCA 18901 CAAGCACGTC TTTCCCAGCA TACATGACGC AGTCCTCTTT GCCCAGGCAA 18951 ATGCTAGAGA CGTGACCCCA GGACACAACT TCCAAGGGGT AAGGTTCTTG 19001 CACCTGGGGA ATCCTAGGCT CCAAGGCACT GAAATAGCAG GACCAAGAGG 19051 CATTATTAGA AAGAACACAG GAGAAGGTTT AAGTTCCAAT ATCAAGTCTG
19101 CCATTTCAGT TTTCTGAATC TGTTTCCTTA TCTATAGAAT GAGCACCATC
19151 AACTAACATT ACCTACCTCT CTGCATTTTT CTTTTATTTT GTTTTAGGGT 19201 TAAATGATAA TTACATCTTT TGTGTCACTT GAAAGCACTT TGTGTATTGT
19251 AAAAATTCTT TATCAATATA AGTTTTCTGG TTGCACAAAC ACCCAAAGCA
19301 TAGTAGAGCA GGCCCACTCT GCTGGCATCG TTCCCTGCCT CCTCCTCATC 19401 CATTITAACT TACCGGAGCT TAGAGATTTC AGGCTGGTGA GGGATAAAGA 19451 GATTGGGTCT GAGTTTTGTC TCAGCTTTTT GACATTTAAT TTACTAGCTC 19501 AGTAAGTCAT ACAAATGGGA TACAAATAAC ACCATCTAAA ACTCCAGAAG 19851 AGAGGGAAAC CCTGGGGAAA CAACGGGCTT TCCTGCTTCG TGAAATTTGT 19901 CCGCAGAGCA AAGAGGGAGA TTCTGGAGGA AGCTGCATTA GTTGTTAGTG
19951 CCCTAATCAT GTTCAGCTAC TCTAGTTGGT ATGTATACTT GATTAGTCAT
20001 AGCACTTATA AATAATTTAT ATTTTATATA ATATATACTT ACATATTATA
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20151 AGATTAGAAA ATAATTCCC AGGAGGACAG GAATTCCCCA AGGTCAGGCA 20201 GCTAGCCAAT AGTTTTTCTA AGCTGAGTAA AACCTTCCCT GCCTCTAACG 20251 GCCCACAAAG GAGGGAAGAC CGCGATACAC ACCTGTCTGG TATAAGGGGG 20301 AAGACCACAG CCGTGCTGTT TTTGTGAGGC AGGTAAGGGA AGGGGCAAGA 20351 GGATAAGTCA TGTGTCAGGA AGCAGCGTCC AACCAGAGCC GGCCACCTGT

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Inventors: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER...

20401 CCCTTTTCCT GCCACCATGC ACCAACTTTG CTGTTCAGTC ACTGAAGCTC 20451 ATTCTGCACT GGCTTCCTCC CTTCCAGGCT CCAGGGGATG CTGAGCTCTC 20501 CTTGTACGAC TCAGAGGAGG ACATTCGCAG CTACTGGGAC TTAGAGCAGG 20551 TGAGCTGAGG GAAGGGGCTG TGAGGGTGGG AGCAGGGCGA AGAGGGGAAG 20601 GATGGGGTCG CTGTCAAATA CAAGGCGTTC ACTCAGCTGT CTCACCTCCA 20651 GCCCAGAGCA GTCACATTCA AGGCCACAAA GATTTGTGGT CATCTTTGTT 20701 TTTTTCTTT TCCTTTTCTT TTTTTTTT TTTTAATTTG AGACAAAGTC 20751 TCACTCTATC ACCCAGACTG GAATGCAGTG GCATGATCTC AGCTCACTGC 20801 AACCTCTGCC TCCCGGGTTC CAGAGGTTCT CCTGCCTCAG CCTCCCGAGT 20851 AGCTGGGACT TCAGGCCTGC GCCCAGCTAA TTTTTGTATT TTTAGTAGAG 20901 ACAGCTTTTC ACCATGTTGG CTGGGCTGGT CTCGAACTTC CGATCTCAAG 20951 CAATCTGCCT GCCTCGGTCT CCTAAGTGCC TGGATTACAG GCATAAGCCA 21001 CGATGCCTGG CCTTTGTTTT CATTCTTCTC ACTCCCTGAA AGGCATCGTG 21051 GGGAGAGGGT GAGTCACTGG ACCAAGTCCT AGAGAACCAG TATCTATTCT 21101 TATTCTCCAA CACATCACCC ACGTGACCCT GAGCAAGCCA CATACACCCT 21151 GGGCCCTAGT TTTTATCATC TGTGAAATTA GGGGAAACAT AGGTAATACC 21201 TGTCCCATCC ACCACACAG ATTGGCAGGG CAGTCACTTG TTCTTTCATT 21251 AATTCAGCAG GTATTTATGG CGTACCTACT GTTTGCCTGA CACAGTTCAG 21301 GATGGGCACA TAGCAGTGAG CAAAACAAAG GCCTCTGCCT TTTAGAAACT 21401 NNNNNNNN NNNNNNNNN NNNNNNGTCT ACAAATGAAT TATTATTGCA 21451 TGTGGACAAG CCTTAAGAAC TAAAAAATAT GTGGCTGGGT GCAATGGTTC 21501 ACACCTGTAA TCCCAGCACT TTGGGAGGCT GAGGTGGGCG GACCACCTGA 21551 GGTCAGGAGT TTGAGACCAG CCTGGCCAAC ATGGCGAAAC CCCGTCTCTA 21601 CTAAAAGCAC AAAAATTAGC CAGGCGTAGT GGTGCATGCC TGTAGTCCCA 21651 GCTACTCGGA AGTCTGAGGC ATGAGAATCA CTTGAACCTG GGAGGCAGAT 21701 GTTGCAGTGA GCCGAGATCG TGCCACTGCA CTCCAGCTTG GGTGACAGAG 21751 CTAGACTGTC TCAAAAACAA ACAAACAAAA CAAAACCTAA AAGATATGTG 21801 GATATGAGGG ATCACCATCC CCATAGGGCC CCTGGATTAA CACCACCCA 21851 CCAATGCCCT GAATTAAAAAG AAACCAGATG ACTAGGTTTG GAGAAATCTG 21901 GCTTTGGGTC TATGAGAAGT AGTGTCTCTC TTTGTGCCTC TTCCCATTCT 21901 GCTTTGGGTC TATGAGAAGT AGTGTCTCTC TTTGTGCCTC TTCCCATTCT
21951 TTTTGACATT GAGCTCCATG GTGCTCTGAA TCCGTCTCTC ACAGTGCTGA
22001 TGGCAGGTGG GACAGATTAG AAAATAGAGC TGGAGCCACA GAGATTTGGC
22051 AGACTGATTT CGGTGCCCTC TTGGAATCTC CAGCACATTC CAAAAAGCCT
22101 GGATAGGACC AAAATAGCTT ATCAACGTGA GAAAGGACTT CAGAGCTTGT
22151 CTACTGCCAA CCCTCATTTT ACCCAATGAG GAAAGGACTT CAGAGCTTGT
22201 GCGAGGGACA CGTGGAAGGT CACACAGCAC ACAGGAGGTG ATTCACATGT
22251 AGATTTCAGC ACCTGCTCT GCCACGCTGG ACTGGTTCAC CTCCTAGGCT
22301 GACCCTGCCT CTCCCCTGTT CACACACACT CTCGCACACA CACACACACA
22351 CACACACACA CACAGGTGCT TTGTTCTGGC CAGGGGTTCC TAGGGTCACC
22401 TCTTGGTTGC AGCCACTGTG ACCCCAACTG GTCTAACCTC TCCTCTCCCC 22401 TCTTGGTTGC AGCCACTGTG ACCCCAACTG GTCTAACCTC TCTCTTCCCC 22451 TCCCACTTCC TTCCTGTGGT TCCTGCAGGA GATGTTCGGG AGCATGTTTC
22501 ACGCAGAGAC CCTGACCGCC CTGTGAGGGC TCAGCCAGTC CTCATGCTGC
22551 CTACAGAGTG CCTGGCACTT GGGACTTCCA TAAAGGATGA GCCTGGGGTC 22601 ACAGGGGGTG TCGGGCGGAG GAAAGTGCAT CCCCCCAGAGC TTGGGTTCCT 22651 CTCTCCTCTC CCCCTCTCT CTCCCTTCCT TCCCTCCCG CATCTCCAGA 22701 GAGAGCCTCT CAGCAGCAGG GGGGTGCTAC CCTTACAGGA GTGAGAGTCT 22701 GAGAGCCTCT CAGCAGGAGG GGGGTGCTAC CCTTACAGGA GTGAGAGTCT 22751 GGTGAGCCCA CTCTTCACCC GTCAGGCCCT GGCCGCAATG GACAAGCCTC 22801 CTGCTCACTC CACCCCACCC ACCTCTGCC TGTCCTTGGC AGCTGAAGGA 22851 CACCTGACT TCCAGCTTTT ACGAGTGAGC CAAAAACAGA AGGACAAGTA 22901 CAACTGTGCT GGCCTGCTGT ACAAGCTTCA AAAAGTGTCC CAGAGCCCAC 22951 ACGGCTCGGT GTCAGATGGT GTCAGGCTGT CACGGACATA GGGATAAACT 23001 TGGTTAGGAC TCTGGCTTGC CTTCCCCAGC TGCCTCAACT CTGTCTCTGG 23051 CAGCTCTGCA CCCAGGGACC ATGTGCTCTC CACACCCAGG AGTCTAGGCC 23101 TTGGTAACTA TGCGCCCCCC GTCCATCATC CCCAAGGCTG CCCAAACCAC
23151 CACTGCTGTC AGCAAGCACA TCAGACTCTA GCCTGGACAG TGGCCAGGAC
23201 CGTCGAGACC ACCAGAGCTA CCTCCCCGGG GACAGCCCAC TAAGGTTCTG
23251 CCTCAGCCTC CTGAAACATC ACTGCCCTCA GAGGCTGCTC CCTTCCCCTG 23301 GAGGCTGGCT AGAAACCCCA AAGAGGGGGA TGGGTAGCTG GCAGAATCAT 23351 CTGGCATCCT AGTAATAGAT ACCAGTTATT CTGCACAAAA CTTTTGGGAA 23401 TTCCTCTTG CACCCAGAGA CTCAGAGGGG AAGAGGGTGC TAGTACCAAC 23451 ACAGGAAAA CGGATGGAC CTGGGCCCAG ACAGTCCCCC TTGACCCCAG
23501 GGCCCATCAG GGAAATGCCT CCCTTTGGTA AATCTGCCTT ATCCTTCTT
23551 ACCTGGCAAA GAGCCAATCA TGTTAACTCT TCCTTATCAG CCTGTGGCCC 23601 AGAGACACAA TGGGTCCTT CTGTAGGCAA AGGTGGAAGT CCTCCAGGGA 23651 TCCGCTACAT CCCCTAACTG CATGCAGATG TGGAAAGGGG CTGATCCAGA 23701 TTGGGTCTTC CTGCACAGGA AGACTCTTTA ACACCCTTAG GACCTCAGGC 23751 CATCTTCTCC TATGAAGATG AAAATAGGGG TTAAGTTTTC CATATGTACA



23801 AGGAGGTATT GAGAGGAACC CTACTGTTGA CTTGAAAATA AATAGGTTCC 23851 ATGTGTAAGT GTTTTGTAAA ATTTCAGTGG AAATGCACAG AAAATCTTCT 23901 GGCCTCTCAT CACTGCTTTT CTCAAGCTTC TTCAGCTTAA CAACCCCTTC 23951 CCTAACAGGT TGGGCTGGCC CAGCCTAGGA AAACATCCCC ATTTCTAACT 24001 TCAGCCAGAC CTGCGTTGTG TGTCTGTGTG TTGAGTGAGC TGGTCAGCTA 24051 ACAAGTCTTC TTAGAGTTAA AGGAGGGGGT GCTGGCCAAG AGCCAACACA 24101 TTCTTGGCCC AGGAGCATTG CTTTTCTGTG AATTCATTAT GCCATCTGGC 24151 TGCCAATGGA ACTCAAAACT TGGAAGGCGA AGGACAATGT TATCTGGGAT 24201 TCACCGTGCA CAGCACCCGA AGTGCCAAAT TCCAGGAGGA CAAGAGCCTT 24251 AGCCAATGAC AACTCACTCT CCCCTACTCC ACCTCCTTCC AAGTCCAGCT 24301 CAGGCCCAGG AGGTGGGAGA AGGTCACAGA GCCTCAGGAA TTTCCAAGTC 24351 AGAGTCCCCT TTGAACCAAG TATCTAGATC CCCTGAGGAC TTGATGAAGT 24401 GATCCTTAAC CCCCAAGTAA TCATTAACCC CCAGACCAGC CTCAGAACTG 24451 AAGGAGATTG TTGACCCAGT GACCTGGAGT TGAGGCTCAG GGAGAGATCT 24501 GCCACATGTC TGAGGGTTGC AGAGCC (SEQ ID NO:3)

FEATURES:

1997 Start: 1997-2121 Exon: Intron: 2122-4732 4733-4872 Exon: 4873-5004 Intron: 5005-5115 Exon: 5116-5781 Intron: 5782-5957 Exon: 5958-7770 Intron: 7771-7935 Exon: 7936-8470 Intron: 8471-8623 Exon: 8624-8917 Intron: Exon: 8918-9000 9001-9777 Intron: 9778-9925 Exon: 9926-10221 Intron: 10222-10335 Exon: 10336-10539 Intron: 10540-10617 Exon: Intron: 10618-11197 11198-11293 Exon: 11294-13338 Intron: 13339-13445 Exon: 13446-14214 14215-14284 Intron: Exon: 14285-14400 Intron: Exon: 14401-14493 14494-15980 Intron: 15981-16262 Exon: Intron: 16263-17597 17598-17652 Exon: 17653-18842 Intron: 18843-18988 Exon: 18989-20477 Intron: 20478-20549 Exon: 20550-22478 Intron: 22479-22523 Exon: Stop: 22524

CHROMOSOME MAP POSITION:

Chromosome 1

ALLELIC VARIANTS (SNPs):

DNA				-	Protein		
	Position	Major	Minor	Domain	Position	Major	<u>Minor</u>
	48	C	G	Beyond ORF(5')		_	
	132	G	Α	Beyond ORF(5')			
	724	Α	C	Beyond ORF(5')			
	1558	C	G	Beyond ORF(5')			
	1228	C	G	Beyond ORF(5')			

FIGURE 3H



1577 2487 2634	A C T	G A C	Beyond ORF(S Intron Intron	5')			
4352	A	C G C T	Intron				
5157	Α	C	Intron				
5658	Α	Т	Intron				
5945	Т	C T	Exon		180	Т	Т
6281	C	Т	Intron		•		
6452	G	C G	Intron				
6610	T	G	Intron				
7247	Ţ	C G	Intron				
7360	A	G	Intron				
7644	A	T C	Intron				
8127 8317	A	A	Intron Intron				
9079	G	A .	Intron				
9537	G	Ť	Intron				
12302	A G G G C C C	A T G T T	Intron				
12354	Č	Ť	Intron				
12487	č	Ť	Intron				
13198	-	À	Intron				
13257	Α	A G	Intron				
14541	G	Α	Intron				
14545	Α	A G	Intron				
15041	C	Α	Intron				
15053	Α	C	Intron				
15065	Α	G	Intron				
15108	Α	Ç	Intron				
16274	-	A C G C G T	Intron				
17424	C	!	Intron		C = 7	.,	.,
17627	G	A	Exon		657	V	٧
18427	T C	<u>C</u>	Intron				
18813 19035	T	G	Intron Intron				
19182	†	2	Intron				
19508	-	GC	Intron				
19571	T	A C G C C G C	Intron				
20147	Τ	Ğ	Intron				
	Ġ	Ä	Intron				
20584	Ä	T	Intron				
20717	T	C	Intron				
20894	Α	G	Intron				
21787	-	A C	Intron				
22264	Т	C	Intron				
22338	-	C C A C	Intron				
23363	Т	C	Beyond ORF(3.)			
23688	G	A C	Beyond ORF(₹; <u>}</u>			
24210	Α	C	Beyond ORF(5 7			

Context:

DNA Position

CTGGGTTCCTATGTGGGGAGGTCATGCTCCCCACTCATTGAGCCCCC

[C,G]

CAGGCAAACCACCTGGACAGCCAGACCCATGCAGACTCTGGAGCAGGTGGAGAGAAGAG TGAGACCACCCCGCCTCACGGGCGGTGAAGGGCCGGCAGCCTCTGAATAGTCTCTGCTAG GAGGTAGAAAGCACCCTCCCATCTTAATCATAGTAATCATCGCCACTACCATTTACTGGG TGCCTATAAAAGGCCAGCCTCTTCATACACATGATCTCACTGAATCCTCATAGCATCTGC CTGCGACTGTTATTATCCCCATTTACAGATGAAGAAACTGAATCTTTGAACCCAGGTCAT

132 CTGGGTTCCTATGTGGGGAGGTCATGCTCCCCACTCATTGAGCCCCCCCAGGCAAACCAC CTGGACAGCCAGACCCATGCAGACTCTGGAGCAGGTGGAGAGGAAGAGTGAGACCACCCC GCCTCACGGGC

[G,A]



ACAGATGAAGAAACTGAATCTTTGAACCCAGGTCATCTGGCTCTCAAACTTGTGCTGTTTTCCCTAAGCCACCCGGTCTCTCATTTCTCCCACTGAAATGTCTCACATGCCATTGCCCTT

ACCCTGTGAGATATGTCTGTTACTCCACTTTATCCATTAACTCATTTGATCTTCACAACA
ACCCTGTGAGATATGTCTGTTACTCCCACTTTAGTGATACAGAATCTGAGGTTTGAAAAG
TAATGCTGACCATTCTGCCTCATTAATAAAAGCAGGATTAACCCAGGCTCCTGGACCCTT
CCACAAAAGGCATTAAGCAACCTGCTCCCCTCTGACAACCTCCCCTGTCACCCAGGCTCT
CCTCTGGGAAGTTGGGGGGCATCTCTAGCCCCCAAGTAGTTACTCATTTTCAACCCCCATCT

2487 ACACGGCTTCTGCACTGGTATCCCTAAGATGGGGTTAAGGGAAGCCCTGGGGAAGTGAGG
TTCTGAATGATGAATTTAAGATCCTACAACCTCATCTGTACTGAGACCCCCAGGGAGGAT
GGGGAGCAGGAGCAAGAACCATCCAGAAGGGTTATATGGCATTCCCAAACCCCTGCATGG
CATCTCCCATATTCTCAATTCACCCGGGTCTCTCTGGGTTTGTTAAGGCATGGTAGATGA
GCATCTACGTTATGGAGGGGTGGGGAGCATCAGAGCCCTTACTCCATGCCCTGTTCCCTC
[C,A]

> ACCAGCGCCCAGGGTCTTTCCACTCTCATCTCCCTGGAAATGCGATGGTGGGTATGAAAC CTTGTCCCTAAGTAGGCGCTACACAAGGTGATCCATACCCACACCCCAGGAGGCTGGGGC TGCGGGTGTCACCCTCCCCATTCCCAGACTCCTGGCAGACCTCCTCTGGCCCAGCTATAG GCCAACTCACTCCCTCACTCCCTTGGGGAAACGGCTGATTCAGTTACCTGGATTGAGG TCACTGGCAATGGCTGAAGTGGAGACGCAGGTGGAACTGGTTCAGGCCGGGGGAATCACC

FIGURE 3J



6281

Docket No.: CL000861
Serial No.: 09/749,589
Inventors: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER...

CAÁGGATGGGAGGTGTGGCAAAGGGGCCTCGGGAGATTTTCCATCTGCATTCTCCTGGAG
TTGTTCCTGGTCAGTCCTAGGGGAATGGTCACTGTGAATGTCATTTCCAGGTCCTCGGTG
ACCTTGGAGAAACCACTGAGCCTCTTTGAGTTCAGTTAGCATTACCTGTTCCATCTTCCT
CCTAGGAATGAGAAGAAGAACTAACCAGAACAAGATATACCATATGCTATAACATGCTTAA
ACAGATGTGAGAAATCACCATCTAACTCCCTGGTTGGTCCCAGCCGGCCACTACAGGGAC

GCTAGAAGGGCATCAGACCACCCTGCCCTCCCTCAAAGCCTTAGCTTTGATGCTAAATC

AAAAAACAACAGCTGTACCTGGTTAAACTGTCCTGAGCTTTAAACCTGTAAAAGACTCAC AGCCTCTCTCCATTATCCCGTGGAGAAACCCAACTCTCTGCCAGCATAGTCTTGCAGACT



GGGCTCACCTCCTCCTCCCCATCCCAGGGCTAAAGTGAACCTTGAAAATTAACAGT ATCTCCTCATCTGCATGTAGCAGGACCATACAAAAAAACAACAGCTGTACCTGGTTAAAC TGTCCTGAGCTTTAAACCTGTAAAAGACTCACAGCCTCTCTCCATTATCCCGTGGAGAAA CCCAACTCTCTGCCAGCATAGTCTTGCAGACTGCTAATTTTCTCTAACATCCCTCACTCC [T,G]

7247 GACACAGAGCAGAGTCACGGAGGACCTCAAAGAGGAGGTGACACTCCACCTCTCTTAAAG
GATGAGAACTTAACCAGGAACAAGGTATACAGAGGATGGTCCAGGCAGAAGGGAACAGTG
CCTAAAAACACTGAGGCCTGAGAGAGTGTGATCTGCGCAGGCAAAGTAAGGGGCTTGGTG
TGGCTGGAGGGTAGAGGGCCCAGAAGAGGGTTGGAAAAGTAGGCAGGAGCCAGACAATGAG
ATCTGGGGTCTGTTCTCTGACAGCGACTTTGGGTCTGATTGGCAGTTTATAAGGATCGTT
[T,C]

GGGCTACACAATGATGAGTGGGAGGTGGATTAGAATCAAGGCAGGGGACCTGTTGGGAGA CTCTGCAGAGGCCCAGGCAGGAATAATGCAGGCGAAGACCAGGTAGAGAAAGAGATGGGG CTGGACTTGAAAAGAATGTTTTACCAGGAGCTTGGTGATAGACTGGATGTGGGAGGTAAG GGAGGATGACTCTCAAGTTTTTGGTTGGGCAACCAGGTTAATGATGGTGTCATTTACTGA GAGAGAAAACACTGGGGGAGGACTAGACTTATTTTACAGATAAGCCAAAGCCAGAGAGGG

7360 AACAGTGCCTAAAAACACTGAGGCCTGAGAGAGTGTGATCTGCGCAGGCAAAGTAAGGGG
CTTGGTGTGGCTGGAGGGTAGAGGGCCCAGAAGAGGATGGAAAAGTAGGCAGAGCCAGA
CAATGAGATCTGGGGTCTGTTCTCTGACAGCGACTTTGGGTCTGATTGGCAGTTTATAAG
GATCGTTTGGGCTACACAATGATGAGTGGGAGGTGGATTAGAATCAAGGCAGGGACCTG
TTGGGAGACTCTGCAGAGGCCCAGGCAGGAATAATGCAGGCGAAGACCAGGTAGAGAAAG
[A,G]

GATGGGGCTGGACTTGAAAAGAATGTTTTACCAGGAGCTTGGTGATAGACTGGATGTGGG AGGTAAGGGAGGATGACTCTCAAGTTTTTGGTTGGCAACCAGGTTAATGATGGTGTCAT TTACTGAGAGAGAAAACACTGGGGGAGGACTAGACTTATTTTACAGATAAGCCAAAGCCA GAGAGGTGATGTGACAGAAAGGCCCATGCTCTAAAGGAGCTGAAGGTCTGATGGCAGCCA TGTAGAGCACAGTGAAGGCAGGTGAAGGTCACAGATGCTCCAATTCCCTCAAGCTACTG

8127 CATCCGGGGCTTCATGACGGCCGCCGGCCTGCAGATCCTGATTTCGGTGCTCAAGTACAT CTTCGGACTGACCATCCCCTCCTACACAGGCCCAGGGTCCATCGTCTTTGTGAGTCTGGG GATGCACCCCTGCCATTGGAGCAAGGCTCCAGCAGACACATGAGGAGGATGTACTGTTTT AAGATGTCGTGAGCTCCTCATTGCAAGGGCTGGCTTAGCTGTTGTTCAGAGAGGATTCTG AGGGGGTTTCTGTCTTGGGAGGGGTCAAAGTCATGACTCACAGAGGTTCTTGGTAGTTAAT [A,C]

FIGURE 3L



THE TOTAL PROPERTY OF THE PARTY OF THE PARTY

CCCCACACCAACATCGCCTCGCTCATCTTCGCTCTCATCAGCGGTGCCTTCCTGGTGCTGGTGAAGGAGCTCAATGCTCGCTACATGCACAAGATTCGCTTCCCCATCCCTACAGAGATG

9079 TTCTACTGCTCTAATAATTCCCCCTAAGGAGGCAGGGGAGTGGGATTCAGGGTCCCCAGA
GAAAAGGGAGACTTGAGAGAGACGCCTGCCCTGGCCCCACCTTAGGGCCAATCCCCATTC
TCCACTCTGGGGTTTGCAGGTGGTGGTGGCAACAGCTATCTCCGGGGGCTGTAAGATGCC
CAAAAAGTATCACATGCAGATCGTGGGAGAAATCCAACGCGGGTGAGTCCAGGTGGCCCA
GAAGCCTGGCCCACCCGCACCTCATGCCCCACTAAGGCCTGAGCTCGGAGAGGGAGACAA

[G,A]
ATGAACTCTATGAAAGTGCAGTCGAAACTGTATGACACTGACCATGTATGAATTATTACT
ATTACCGTTTCCTGAGAAGGGCCGCACAACCAGCCAATGTAGGCTATTTTATGAGAAATG
AGTCTTAACTGCCACACTCCCCTTATAAATCTCATTCAACTGATGCTGTTAAACAAAGCC
TCTCTGAACAGCCGCTTGCTGGCTCTTTGCCTTGCTCTAATGCATTGGTTCTTTGTCCAT
GTAGAAAGGGAACTATTAGGTTCAACCAGATTCATGAAGCATCCACTCTGTGCCAGGCAC

9537 AACTGATGCTGTTAAACAAAGCCTCTCTGAACAGCCGCTTGCTGGCTCTTTTGCCTTGCTC
TAATGCATTGGTTCTTTGTCCATGTAGAAAGGGAACTATTAGGTTCAACCAGATTCATGA
AGCATCCACTCTGTGCCAGGCACCATGCTGGGCCCTGGGAGGAGAGGGGTGACGCTTGTC
CTGCAGGGTTGGAACAGGCAAGGGAGGGAAGACCACATAGCACCAAAAGGTCTAGGGGTCT
GTGGACTCGTGAGCATACAGGGTTCAGAATCTGGGAGTTAACAAACGAGGCCCTACCACA
[G,T]

12354 GAAACCAAGGCTCAGAATGGTTAAGTAAATTGTCAAAGGCCACAGAGGTAGGGAGTGGTA
GAGTCTGGATTAAAACTCCAAGTCCTGGACTCCAGACCTCTAGGCTGTACTGTCTCATAG
GGAAGGCAGTCTCACCCACCTAGGGCAGAGAAAAATCCTTAAAGCCAGAGAAGTGAGT
GGCTCATCTGTGGTCACCCAGAGAGACAGTGATGAGGACAGGGAGAAAAATTATACCTCA
GTTCCCAGCCCAAGGATCTGCTTTGACCATAACCCAACAAGCCCCCGCTATGGTGGTATT
[C,T]

FIGURE 3M



[-,A]
AAAATGCTATTTAAAGAAAAAAAGAGAAGAGAGGCTCTGAGGTTGTACTAACAGAGAAT
GGCCTTGGCTAATCCAGGAAGACTTCCTGAAAGAGGTTGTTTTTTTCCCCAGGTCTGCTTT
TGACATCTCTCTTTTCACAGTGCATCTGGGTAGTGAGCTTCCTCCTCCTTCTTCCTCA
GCCTGCCCTATGGTGTGGCAGTGGGTGTCGCCTTCTCCGTCCTGGTCGTCGTCGTCAGA
CTCAGTTGTAAGTGATAGCTTCCGCCCTCCTAGGCCCACAGTCGGTTCCCTGGGCCAGCC

TGGCCTTGGCTAATCCAGGAAGACTTCCTGAAAGAGGTTGTTTTTTCCCCAGGTCTGCTT
TTGACATCTCTCTTTTCACAGTGCATCTGGGTAGTGAGCTTCCTCCTCCTCCTCCTCCTC
AGCCTGCCCTATGGTGTGGCAGTGGGTGTCGCCTTCTCCGGTCGTCGTGGTCTTCCAG
ACTCAGTTGTAAGTGATAGCTTCCGCCCTCCTAGGCCCACAGTCGGTTCCCTGGGCCAGC
CCGCAAAGGGCTTCCATGCCACGGCCTGGCTTAGTCCACCTTCCACCTCTGGGCC

CTTGGATGAGGTGCTACCATCTCCCAGGGAAGCCACTGAACCCCCAAGGCCCTTCTCCAT TTTCTGGCTAAGATAGGACATGGCCCATGGACTTTTGAACAACCCAGAGGGGGAACAGCA

15065 CAGCCCCGTGCCCTGCTCTCCTGCCCATTCTGATACTGCCCCCTGTTACTCATGGTACCC



CCCAGCTAATTTTTGTATTTTTAGTAGATATTGGGTTTCACCATGTTGGCCAGGCTGGTG
TCAAACTCCTGACCTCAGGTGATCCACCTACCTTAGCCTTCCAAAGTGCTGGGATTACAA
GCCTGAGCCACTGCGCCCAGCCTGGGCATTTTTCTTCTTGGATGAGGTGCTACCATCTCC
CAGGGAAGCCACTGAACCCCCAAGGCCCTTCTCCATTTTCTGGCTAAGATAGGACATGGC
CCATGGACTTTTGAACAACCCAGAGGGGGAACAGCAGTGAATTTCCTGGGGAACCCAGGC

- GGGTGCATATACACAGCCTCAAGGACGTGGCCACAGGGCAGCAGACATTTACATGACTAG
 CATGTACGCAAAGTGCAGAGATGTGGGAGCAAGTGCACACAGACACACAGAGAATGTGA
 AGGGGCACATACACACACCCCAGCTCCCTGCACTGGGTCAGACCCCCTCCAGCAGGGCT
 GCAGTTCCCAAGCTCCGCATGGCCACGTTCGGGGAGAGAATCTGCAGTGGCAATGACCTG
 CTATGATATGTTCTGGAGTTAGAAGCAGTGGATTCTCCCCAACCTCACTGGACACCCCCT
 [T, C]
 AGGAAACCATCTCTAGGATTAAGAGTAATCCACACAAACTTCCAATGCCACACATTGGAA
 GTTGCTGGAAAGGTCTGGGAAAACAAGAGGAAGGATGGTCCTTGGGGGATAGAACTGGC
 AGCGGCCTCTTCAAGGATGGCTTAGGCTTTTCCACTCGAATCACACAAAGTACTGACTC

FIGURE 30



CCTAAATCAAACTGCTTCCTTCTGCTCTGGGTTGAAACTTCAGCATCCTCAAGTTCATGT TGCCCTCTGCCGTCCAGAACTGATATTGCACTGCCAATGCCATGGCCCTCAGATACAGCA

TTTCTGAAGGTGATCTTTTCTCCTTCTAGCCCAGGTGTACAATGACATTAGCCATGGAGG CGTCTTTGAGGATGGGAGTCTAGAATGCAAGCACGTCTTTCCCAGCATACATGACGCAGT CCTCTTTGCCCAGGCAAATGCTAGAGACGTGACCCCAGGACACAACTTCCAAGGGGTAAG GTTCTTGCACCTGGGGAATCCTAGGCTCCAAGGCACTGAAATAGCAGGACCAAGAGGCAT TATTAGAAAGAACACAGGAGAAGGTTTAAGTTCCAATATCAAGTCTGCCATTTCAGTTTT

19035 GGACCTCAGGCCTCTCCCATCCCTGCTCTGGTCTCACTATCTTCCCCACCCCCAGCTCCA
ATCCACAATGGCTGTTATCTTTCTGAAGGTGATCTTTTCTCCTTCTAGCCCAGGTGTACA
ATGACATTAGCCATGGAGGCGTCTTTGAGGATGGAGATTCAGAATGCAAGCACGTCTTTC
CCAGCATACATGACGCAGTCCTCTTTGCCCAGGCAAATGCTAGAGACGTGACCCCAGGAC
ACAACTTCCAAGGGGTAAGGTTCTTGCACCTGGGGAATCCTAGGCTCCAAGGCACTGAAA
[T,C]

ÁGCAGGACCAAGAGGCATTATTAGAAAGAACACAGGAGAAGGTTTAAGTTCCAATATCAA
GTCTGCCATTTCAGTTTTCTGAATCTGTTTCCTTATCTATAGAATGAGCACCATCAACTA
ACATTACCTACCTCTCTGCATTTTTCTTTTATTTTGTTTTAGGGTTAAATGATAATTACA
TCTTTTGTGTCACTTGAAAGCACTTTGTGTATTGTAAAAATTCTTTATCAATATAAGTTT
TCTGGTTGCACAAACACCCCAAAGCATAGTAGAGCAGGCCCACTCTGCTGGCATCGTTCCC

FIGURE 3P



> GAATTCCCCAAGGTCAGGCAGCTAGCCAATAGTTTTTCTAAGCTGAGTAAAACCTTCCCT GCCTCTAACGGCCCACAAAGGAGGGAAGACCGCGATACACACCTGTCTGGTATAAGGGGG AAGACCACAGCCGTGCTGTTTTTGTGAGGCAGGTAAGGGAAGGGGCAAGAGGATAAGTCA TGTGTCAGGAAGCAGCGTCCAACCAGAGCCGGCCACCTGTCCCTTTTCCTGCCACCATGC ACCAACTTTGCTGTTCAGTCACTGAAGCTCATTCTGCACTGGCTTCCTCCCTTCCAGGCT

> AGACTGGAATGCAGTGGCATGATCTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCCAGA
> GGTTCTCCTGCCTCAGCCTCCGAGTAGCTGGGACTTCAGGCCTGCGCCCAGCTAATTTT

TAAAAGATATGTGGATATGAGGGATCACCATCCCCATAGGGCCCCTGGATTAACACCACC CCACCAATGCCCTGAATTAAAAGAAACCAGATGACTAGGTTTTGGAGAAATCTGGCTTTTGG GTCTATGAGAAGTAGTGTCTCTTTTTGTGCCTCTTTCCCATTCTTTTTTGACATTGAGACTCC ATGGTGCTCTGAATCCGTCTCTCACAGTGCTGATGGCAGGTGGGACAGATTAGAAAATAG AGCTGGAGCCACAGAGATTTGGCAGACTGATTTCGGTGCCCTCTTTGGAATCTCCAGCACA

22264 CTCCATGGTGCTCTGAATCCGTCTCTCACAGTGCTGATGGCAGGTGGGACAGATTAGAAA

FIGURE 3Q



ATAGAGCTGGAGCCACAGAGATTTGGCAGACTGATTTCGGTGCCCTCTTGGAATCTCCAG CACATTCCAAAAAGCCTGGATAGGACCAAAATAGCTTATCAACGTGAGAAAGGACTTCAG AGCTTGTCTACTGCCAACCCTCATTTTACCCAATGAGGAAAGTGAAGCTATTAGGGGGCG AGGGACACGTGGAAGGTCACACAGCACACAGGAGGTGATTCACATGTAGATTTCAGCACC [T,C]

ĞCTCCTGCCACGCTGGACTGGTTCACCTCCTAGGCTGACCCTGCCTCTCCCCTGTTCACA
CACACTCTCGCACACACACACACACACACACACACAGGTGCTTTGTTCTGGCCAGG
GGTTCCTAGGGTCACCTCTTGGTTGCAGCCACTGTGACCCCAACTGGTCTAACCTCTCT
TTCCCCTCCCACTTCCTTCCTGTGGTTCCTGCAGGAGATGTTCGGGAGCATGTTTCACGC
AGAGACCCTGACCGCCCTGTGAGGGCTCAGCCAGTCCTCATGCTGCCTACAGAGTGCCTG

CACACACACACACACACACACACAGGTGCTTTGTTCTGGCCAGGGGTTCCTAGGGTCA
CCTCTTGGTTGCAGCCACTGTGACCCCAACTGGTCTAACCTCTCTTCCCCTCCCACTT
CCTTCCTGTGGTTCCTGCAGGAGATGTTCGGGAGCATGTTTCACGCAGAGACCCTGACCG
CCCTGTGAGGGCTCAGCCAGTCCTCATGCTGCCTACAGAGTGCCTGGCACTTGGGACTTC
CATAAAGGATGAGCCTGGGGTCACAGGGGGTGTCGGGCGGAGAAAGTGCATCCCCCAGA

AATAGATACCAGTTATTCTGCACAAAACTTTTGGGAATTCCTCTTTGCACCCAGAGACTC
AGAGGGGAAGAGGGTGCTAGTACCAACACAGGGAAAACGGATGGGACCTGGGCCCAGACA
GTCCCCCTTGACCCCAGGGCCCATCAGGGAAATGCCTCCCTTTGGTAAATCTGCCTTATC
CTTCTTTACCTGGCAAAGAGCCAATCATGTTAACTCTTCCTTATCAGCCTGTGGCCCAGA
GACACAATGGGGTCCTTCTGTAGGCAAAGGTGGAAGTCCTCCAGGGATCCGCTACATCCC

AAACTTTTGGGAATTCCTCTTTGCACCCAGAGACTCAGAGGGGAAGAGGGTGCTAGTACC
AACACAGGGAAAACGGATGGGACCTGGGCCCAGACAGTCCCCCTTGACCCCAGGGCCCAT
CAGGGAAATGCCTCCCTTTGGTAAATCTGCCTTATCCTTCTTTACCTGGCAAAGAGCCAA
TCATGTTAACTCTTCCTTATCAGCCTGTGGCCCAGAGACACAATGGGGTCCTTCTGTAGG
CAAAGGTGGAAGTCCTCCAGGGATCCGCTACATCCCCTAACTGCAGATGTGGAAAG
[G,A]

GGCTGATCCAGATTGGGTCTTCCTGCACAGGAAGACTCTTTAACACCCTTAGGACCTCAG
GCCATCTTCTCCTATGAAGATGAAAATAGGGGTTAAGTTTTCCATATGTACAAGGAGGTA
TTGAGAGGAACCCTACTGTTGACTTGAAAATAAATAGGTTCCATGTGTAAGTGTTTTGTA
AAATTTCAGTGGAAATGCACAGAAAATCTTCTGGCCTCTCATCACTGCTTTTCTCAAGCT
TCTTCAGCTTAACAACCCCTTCCCTAACAGGTTGGGCTGGCCCAGCCTAGGAAAACATCC

TCACTGCTTTTCTCAAGCTTCTTCAGCTTAACAACCCCTTCCCTAACAGGTTGGGCTGGC
CCAGCCTAGGAAAACATCCCCATTTCTAACTTCAGCCAGACCTGCGTTGTGTGTCTGTGT
GTTGAGTGAGCTAGCTAACAAGTCTTCTTAGAGTTAAAGGAGGGGGTGCTGGCCAA
GAGCCAACACATTCTTGGCCCAGGAGCATTGCTTTTCTGTGAATTCATTATGCCATCTGG
CTGCCAATGGAACTCAAAACTTGGAAGGCGAAGGACAATGTTATCTGGGATTCACCGTGC
[A,C]

FIGURE 3R